

FIGURE 1

FOOTEST 200T

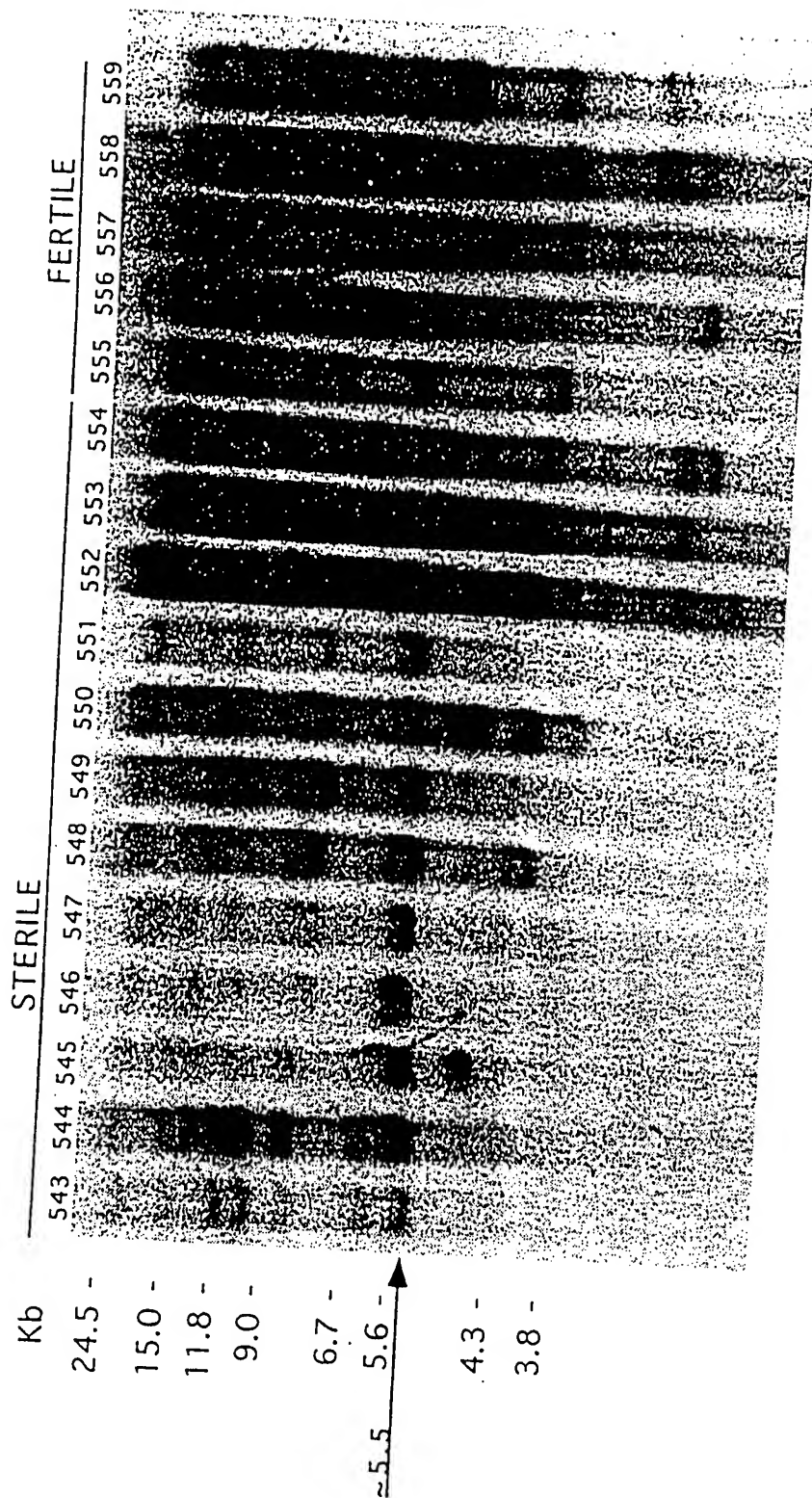


FIGURE 2

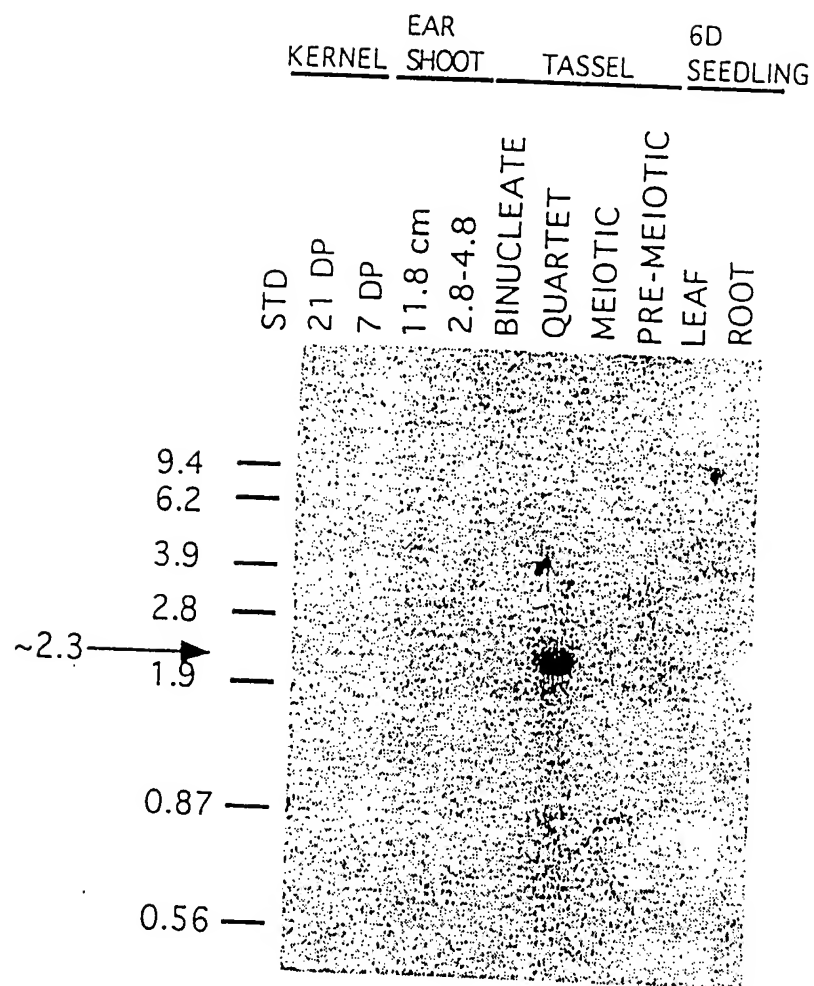


FIGURE 3

Figure 4

EcoRI
|
GAATTCGGCAGGAGGAAGCTCACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTA
1 -----+-----+-----+-----+-----+ 60
CTTAAGCCGTGCTCCCTTCGAGTGGAGTGC GGCCGCTGCGGTAGCGGTAAGAAGGGTGAT
a E F G T R E A H L T P A T P S P F F P L -
GCAGGGCCTCACAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAG
61 -----+-----+-----+-----+-----+ 120
CGTCCCGGAGTGTTTCATGTAGCGCGAGGAAGACCAACAGGAGAGTACCTAGGACCAGGTC
a A G P H K Y I A L L L V V L S W I L V Q -
AGGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGCGCAACGGTG
121 -----+-----+-----+-----+-----+ 180
TCCACCTCGGACTCCTTCGTCTTTCCGGGCTCTAGTACCGGTCACTAGCCGCGTTGCCAC
a R W S L R K Q K G P R S W P V I G A T V -
GAGCAGCTGAGGAAGTACCACCGGATGCACGACTGGCTTGTCGGGTACCTGTACGGCAC
181 -----+-----+-----+-----+-----+ 240
CTCGTCGACTCCTTGATGGTGGCCTACGTGCTGACCGAACAGCCCATGGACAGTGCCGTG
a E Q L R N Y H R M H D W L V G Y L S R H -
AGGACAGTGACCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT
241 -----+-----+-----+-----+-----+ 300
TCCTGTCACTGGCAGCTGTACGGCAAGTGAAGGATGTGGATGTAGCGACTGGGCCACTTA
a R T V T V D M P F T S Y T Y I A D P V N -
GTCGAGCATGTCCTCAAGACTAACTTCACCAATTACCCCAAGGGAATCGTGTACAGATCC
301 -----+-----+-----+-----+-----+ 360
CAGCTCGTACAGGAGTTCTGATTGAAGTGGTTAATGGGGTTCCTTAGCACATGTCTAGG
a V E H V L K T N F T N Y P K G I V Y R S -
TACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCGACGGCGAGCTGTGGAGGAAG
361 -----+-----+-----+-----+-----+ 420
ATGTACCTGCACGAGGAGCCACTGCCGTAGAAGTTGCGGCTGCCGCTCGACACCTCCTTC
a Y M D V L L G D G I F N A D G E L W R K -
CAGAGGAAGACGGCGAGTTTCGAGTTCGCCTCCAAGAACCTGAGGGATTTTCAGCGCCATT
421 -----+-----+-----+-----+-----+ 480
GTCTCCTTCTGCCGCTCAAAGCTCAAGCGAGGTTCTTGACTCCCTAAAGTCGCGGTAA
a Q R K T A S F E F A S K N L R D F S A I -

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Figure 4B

GTGTTTCAGAGAGTACTCCCTGAAGCTGTCCGGTATACTGAGCCAGGCATCCAAGGCAGGC
 481 -----+-----+-----+-----+-----+-----+ 540
 CACAAGTCTCTCATGAGGGACTTCGACAGCCCATATGACTCGGTCCGTAGGTTCCGTCCG
 a V F R E Y S L K L S G I L S Q A S K A G -
 AAAGTTGTGGACATGCAGGAACCTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT
 541 -----+-----+-----+-----+-----+ 600
 TTTCAACACCTGTACGTCTTGAATGTACTCCTACTGCGACCTGAGGTAGACGTTCCAA
 a K V V D M Q E L Y M R M T L D S I C K V -
 GGGTTCGGGGTCGAGATCGGCACGCTGTGCCAGATCTCCCCGAGAACAGCTTCGCGCAG
 601 -----+-----+-----+-----+-----+ 660
 CCCAAGCCCCAGCTCTAGCCGTGCGACAGCGGTCTAGAGGGGCTCTTGTGAAGCGCGTC
 a G F G V E I G T L S P D L P E N S F A Q -
 GCGTTCGATGCCGCCAACATCATCATCAGCTGCGGTTTCATCGACCCGCTGTGGCGCATC
 661 -----+-----+-----+-----+-----+ 720
 CGCAAGCTACGGCGGTTGTAGTAGTAGTGCGACGCCAAGTAGCTGGGCGACACCGCGTAG
 a A F D A A N I I I T L R F I D P L W R I -
 AAGAGGTTCTTCCACGTCCGGTCAGAGGCCCTCCTAGCGCAGAGCATCAAGCTCGTGGAC
 721 -----+-----+-----+-----+-----+ 780
 TTCTCCAAGAAGGTGCAGCCCAGTCTCCGGGAGGATCGCGTCTCGTAGTTCGAGCACCTG
 a K R F F H V G S E A L L A Q S I K L V D -
 GAGTTCACCTACAGCGTGATCCGCCGAGGAAGGCCGAGATCGTCGAGGTCCGGGCCAGC
 781 -----+-----+-----+-----+-----+ 840
 CTCAAGTGATGTGCGACTAGGCGGCCTCCTTCCGGCTCTAGCAGCTCCAGGCCCGGTCCG
 a E F T Y S V I R R R K A E I V E V R A S -
 GGCAAACAGGAGAAGATGAAGCACGACATCCTGTACGGTTCATCGAGCTGGGCGAGGCC
 841 -----+-----+-----+-----+-----+ 900
 CCGTTTGTCTCTTCTACTTCTGCTGTAGGACAGTGCCAAGTAGCTCGACCCGCTCCGG
 a G K Q E K M K H D I L S R F I E L G E A -
 GGCGACGACGGCGGCGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTGCTCAACTTC
 901 -----+-----+-----+-----+-----+ 960
 CCGCTGCTGCCGCCGCCGAAGCCCCTGCTATTCTCGGAGGCCCTGCACCACGAGTTGAAG
 a G D D G G G F G D D K S L R D V V L N F -
 GTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTGCTGGTTCACGCACATGGCCATG
 961 -----+-----+-----+-----+-----+ 1020
 CACTAGCGGCCCCCCTGTGCTGCCGCTGCTGCGACAGCACCAAGTGCCTGTACCGGTAC
 a V I A G R D T T A T T L S W F T H M A M -

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Figure 4C

TCCCACCCGGACGTGGCCGAGAAGCTGCGCCGCGAGCTGTGCGCGTTTCGAGGCGGAGCGC
 1021 -----+-----+-----+-----+-----+ 1080
 AGGGTGGGCCTGCACCGGCTCTTCGACGCGGCGCTCGACACGCGCAAGCTCCGCCTCGCG
 a S H P D V A E K L R R E L C A F E A E R -
 GCGCGCGAGGAGGGCGTCACGCTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCG
 1081 -----+-----+-----+-----+-----+ 1140
 CGCGCGCTCCTCCCGCAGTGCGAGCACGAGACGCCGCCGCGACTGCGGCTGCTGTTCCGC
 a A R E E G V T L V L C G G A D A D D K A -
 TTCGCCGCCCCGCGTGGCGCAGTTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTG
 1141 -----+-----+-----+-----+-----+ 1200
 AAGCGGCGGGCGCACCGCGTCAAGCGCCCGGAGGAGTGATGCTGTGCGAGCCGTTTCGAC
 a F A A R V A Q F A G L L T Y D S L G K L -
 GTCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTCCTCAGGAC
 1201 -----+-----+-----+-----+-----+ 1260
 CAGATGGAGGTGCGGACGCGAGTGGCTCTGCGAGGCGGACATGGGGCGGCAGGGAGTCTTG
 a V Y L H A C V T E T L R L Y P A V P Q D -
 CCAAGGGGATCCTGGAGGACGACGTGCTGCCGACGGGACGAAGGTGAGGGCCGCGGG
 1261 -----+-----+-----+-----+-----+ 1320
 GGGTTCCTTAGGACCTCCTGCTGCACGACGGCCTGCCCTGCTTCCACTCCCGGCCGCC
 a P K G I L E D D V L P D G T K V R A G G -
 ATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGTACAAGTGGGGCCCCGACGCG
 1321 -----+-----+-----+-----+-----+ 1380
 TACCACTGCATGCACGGGATGAGCTACCCCGCCTACCTCATGTTGACCCCGGGGCTGCGC
 a M V T Y V P Y S M G R M E Y N W G P D A -
 GCGAGCTTCCGGCCGAGCGGTGGATCAACGAGGATGGCGCGTTCCGCAACGCGTCGCCC
 1381 -----+-----+-----+-----+-----+ 1440
 CGCTCGAAGGCCGCGCTCGCCACCTAGTTGCTCCTACCGCGCAAGGCGTTGCGCAGCGGC
 a A S F R P E R W I N E D G A F R N A S P -
 TTCAAGTTCACGGCGTTCCAGGCGGGCCGAGGATCTGCCTGGGCAAGGACTCGGCGTAC
 1441 -----+-----+-----+-----+-----+ 1500
 AAGTTCAAGTGCCGCAAGGTCCGCCCCGCTCCTAGACGGACCCGTTCTGAGCCGCATG
 a F K F T A F Q A G P R I C L G K D S A Y -
 CTGCAGATGAAGATGGCGCTGGCCATCCTCTTCCGCTTCTACAGCTTCCGGCTGCTGGAG
 1501 -----+-----+-----+-----+-----+ 1560
 GACGTCTACTTCTACCGCGACCGGTAGGAGAAGGCGAAGATGTGCAAGGCCGACGACCTC
 a L Q M K M A L A I L F R F Y S F R L L E -

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Figure 4D

GGGCACCCGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGGCCTCAAGGTC
 1561 -----+-----+-----+-----+-----+-----+-----+ 1620
 CCCGTGGGCCACGTCATGGCGTACTACTGGTAGGAGAGGTACCGCGTGCCGGAGTTCCAG

a G H P V Q Y R M M T I L S M A H G L K V -

CGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATATGGATATCGTCCCGCTTAAT
 1621 -----+-----+-----+-----+-----+-----+ 1680
 GCGCAGAGATCCCGGCAGACTACAGTACCGCTAAACCTATACCTATAGCAGGGCGAATTA

a R V S R A V * C H G D L D M D I V P L N -

CCACGACAAATAACGCTCGTGTTACAAATTTGCATGCATGCATGTAAGGGAAAGCGATGG
 1681 -----+-----+-----+-----+-----+-----+ 1740
 GGTGCTGTTTATTGCGAGCACAATGTTTAAACGTACGTACGTACATTCCCTTTGCTACC

a P R Q I T L V L Q I C M H A C K G K R W -

GTTTCATTGGTGGCTTGGCTTAAGCCTTAAAACTCCGTCGGGTCTTGCGAACCACCACA
 1741 -----+-----+-----+-----+-----+-----+ 1800
 CAAAGTAACCACCGAACCGAATTCGGAATTTTGGAGGCAGCCCAGAACGCTTGGTGGTGT

a V S L V A W L K P *

TCACTAGTGTGTTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC
 1801 -----+-----+-----+-----+-----+-----+ 1860
 AGTGATCACAAAACATGAGATGAGGAGTCACCTTCACATCACTGTCGTATGTTCAAGTAG

XhoI
 |

ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAAAACTCGAG
 1861 -----+-----+-----+-----+-----+-----+ 1906
 TATATATAATAGGAGAAAGAATTTTTTTTTTTTTTTTTTTTGGAGCTC

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1 GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC
51 GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCA GGGATGGCAA
101 TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA
151 GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC
201 AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT
251 GTCACCTCCTA CTTTATTCTT TGGTTGGGCA ACTTCCAATA GGCTCATGTT
301 AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT
351 ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT
401 TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA
451 ATTTTCTCAG TTTGGTCCAT GTAATTTTTG AAGTGAGGTT CCTTAAATTT
501 CATTATGCTT CCTTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACCT
551 TGGGTTCACA AATTGACTCA CAAGAAAACA AATTCACCTT TGGGTTCACA
601 AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA
651 AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT
701 CTTTCTGGTT GGTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC
751 AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT
801 AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA
851 GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA
901 GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTTGG GGTACACCA
951 AGATTGTCTC TCTCGAGGTT GGGGGGTCCC TAAGGTTGGT AGTAGCAATA
1001 CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA
1051 TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACCAT GGAGGAAGCT
1101 CACATCACGC CGGCGACGCC ATCGCCATTC TTCCCACTAG CAGGGCCTCA
1151 CAAGTACATC GCGCTCCTCC TGGTTGTCCT CTCATGGATC CTGGTCCAGA
1201 GGTGGAGCCT GAGGAAGCAG AAAGGCCCCG GATCATGGCC AGTCATCGGT
1251 GCAACGGTGG AGCAGCTGAG GAACTACCAC CGGATGCACG ACTGGCTTGT
1301 CGGGTACCTG TCACGGCACA GGACAGTGAC CGTCGACATG CCGTTCACCT
1351 CCTACACCTA CATCGCTGAC CCGGTGAATG TCGAGCATGT CCTCAAGACT

Figure 5B

1401 AACTTCACCA ATTACCCCAA GGTAATGAC CTGAACTCAC TGATGTTTCAG
1451 TCTTCGGAAA TCAGAGCTGA AAGCTGAATC GAATGTGCCT GAACACCGTG
1501 TAGGGAATCG TGTACAGATC CTACATGGAC GTGCTCCTCG GTGACGGCAT
1551 CTTCAACGCC GACGGCGAGC TGTGGAGGAA GCAGAGGAAG ACGGCGAGTT
1601 TCGAGTTCGC CTCCAAGAAC CTGAGGGATT TCAGCGCCAT TGTGTTTCAGA
1651 GAGTACTCCC TGAAGCTGTC GGGTATACTG AGCCAGGCAT CCAAGGCAGG
1701 CAAAGTTGTG GACATGCAGG TGAGATCACT GCTCCCTTGC CATTGCCAAC
1751 ATGAGCATTT CAACCTGAGA CACGAGAGCT ACCTTGCCGA TTCAGGAACT
1801 TTACATGAGG ATGACGCTGG ACTCCATCTG CAAGGTTGGG TTCGGGGTTCG
1851 AGATCGGCAC GCTGTCGCCC GATCTCCCCG AGAACAGCTT CGCGCAGGCG
1901 TTCGATGCCG CCAACATCAT CGTCACGCTG CGGTTTCATCG ACCCGCTGTG
1951 GCGCATCAAG AGGTTCTTCC ACGTCGGGTC AGAGGCCCTC CTAGCGCAGA
2001 GCATCAAGCT CGTGGACGAG TTCACCTACA GCGTGATCCG CCGGAGGAAG
2051 GCCGAGATCG TCGAGGCCCC GGCCAGCGGC AAACAGGAGA AGGTACGTGC
2101 ACATGACTGT TTCGATTCTT CAGTTCATCG TCTTGGCCGG GATGGACCTG
2151 ATCCTGATTG ATTATATATC CGTGTGACTT GTGAGGACAA ATTAAAATGG
2201 GCAGATGAAG CACGACATCC TGTCACGGTT CATCGAGCTA GGCGAGGCCG
2251 GCGACGACGG CGGCGGCTTC GGGGACGACA AGAGCCTCCG GGACGTGGTG
2301 CTCAACTTCG TGATCGCCGG GCGGGACACG ACGGCGACGA CGCTGTCTGTG
2351 GTTCACGCAC ATGGCCATGT CCCACCCGGA CGTGGCCGAG AAGCTGCGCC
2401 GCGAGCTGTG CGCGTTCGAG GCGGAGCGCG CGCGCGAGGA GGGCGTCGCG
2451 CTCGTGCCCT GCGGCGGCGC TGACGCCGAC GACAAGGCGT TCGCCGCCCG
2501 CGTGGCGCAG TTCGCGGGCC TCCTCACCTA CGACAGCCTC GGCAAGCTGG
2551 TCTACCTCCA CGCCTGCGTC ACCGAGACGC TCCGCTGTA CCCC GCCGTC
2601 CCTCAGGTGA GCGCGCCCCG CACGCGACCT CCGGTCCAGA GCACAGCATG
2651 CAGTGAGTGG ACCTGAATGC AATGCACATG CACTTGCGCG CGCGCAGGAC
2701 CCCAAGGGGA TCCTGGAGGA CGACGTGCTG CCGGACGGGA CGAAGGTGAG
2751 GGCCGGCGGG ATGGTGACGT ACGTGCCCTA CTCGATGGGG CGGATGGAGT

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Figure 5C

2801 ACAACTGGGG CCCCACGCG GCGAGCTTCC GGCCGGAGCG GTGGATCAAC
2851 GAGGATGGCG CGTTCCGCAA CGCGTCGCCG TTCAAGTTCA CGGCGTTCCA
2901 GGCGGGGCGG AGGATCTGCC TGGGCAAGGA CTCGGCGTAC CTGCAGATGA
2951 AGATGGCGCT GGCCATCCTC TTGCGCTTCT ACAGCTTCCG GCTGCTGGAG
3001 GGGCACCCGG TGCAGTACCG CATGATGACC ATCCTCTCCA TGGCGCACGG
3051 CCTCAAGGTC CGCGTCTCTA GGGCCGTCTG ATGTCATGGC GATTTGGGAT
3101 ATCATCCCGC TTAATCCTTA AAAATTTGCA TGCATGCATG TAAGGGAAAG
3151 CGATGGGTTT CATTGGTGGC TTGGCTTAAG CCTTAAAAAC TCCGTCGGGT
3201 CTTGCGAACC ACCACATCAC TAGTGTTTTG TACTCTACTC CTCAGTGGAA
3251 GTGTAGTGAC AGCATACAAG TTCATCATAT ATATTATCCT CTTTCTTCGC
3301 CGGATGCTTC CCGGGACCTT TTGGAGACCA TTAGTGACAG GCGTGTGAAA
3351 AAAAGGCTTC TTCTGCGGCG AAGTTTTGGG TTCAGAGTCT TGGCGTCTTT
3401 GCAGCAGAAA AAAGGTTTGG AAGGATCTGA ACCCTGAACC GAAAATGGCT
3451 TCGGAAATAT GCTCGCATCG GGGCGGGGCC GTCCTCGGG ATGACGACAA
3501 GCCCACAAGC AGTGAGAGCG AAGCGATCTT TGGAGTTTGG AGACACTCTC
3551 GGACCCCTCG GCGCTCCGCG AGCTCATCTT CGCCTCCTCT GTCGTGTCCG
3601 TGGCGGCACC GCGCCCGCCC GCCTCGTGTT CGACCAAATC CCGCGCCCCG
3651 ACCGGTTCGT GTACAACACC CTCATCCGCG GCGCCGCGCG CAGTGACACG
3701 CCCCAGGACG CCGTATACAT CTATAAATCA TGGTATTGTA CTTTATTTTC
3751 AAACGGCCTT AACACAACCA TATTTTTATG GTAAACACGT TCAAAATTGA
3801 CACAAATTTA AAACAGGCAC AAACCGTAGC TAAACATAAG AGAATGAGAG
3851 ACAACCCAAA GGTTAGAGAT GAAATAAGCT GAGTAAACGA CGAATTC

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Figure 6

1051 TCCATCACTTGTAGACTGGACCCTTCATCAAGAGCACCATGGAGGAAGCT 1100
 1GAATTCGGCACGAGGGAAGCT 21
 1101 CACATCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 1150
 22 CACCTCACGCCGGCGACGCCATCGCCATTCTTCCCACTAGCAGGGCCTCA 71
 1151 CAAGTACATCGCGCTCCTCCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 1200
 72 CAAGTACATCGCGCTCCTTCTGGTTGTCCTCTCATGGATCCTGGTCCAGA 121
 1201 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGT 1250
 122 GGTGGAGCCTGAGGAAGCAGAAAGGCCCGAGATCATGGCCAGTCATCGGC 171
 1251 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 1300
 172 GCAACGGTGGAGCAGCTGAGGAACTACCACCGGATGCACGACTGGCTTGT 221
 1301 CGGGTACCTGTACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 1350
 222 CGGGTACCTGTACGGCACAGGACAGTGACCGTCGACATGCCGTTCACTT 271
 1351 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 1400
 272 CCTACACCTACATCGCTGACCCGGTGAATGTCGAGCATGTCCTCAAGACT 321
 1401 AACTTCACCAATTACCCCAAGGTAAATGACCTGAACTCACTGATGTTTCA 1450
 322 AACTTCACCAATTACCCCA..... 340
 1501 TAGGGAATCGTGACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 1550
 341 .AGGGAATCGTGACAGATCCTACATGGACGTGCTCCTCGGTGACGGCAT 389
 1551 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 1600
 390 CTTCAACGCCGACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTT 439
 1601 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTAGCGCCATTGTGTTCAGA 1650
 440 TCGAGTTCGCCTCCAAGAACCTGAGGGATTTAGCGCCATTGTGTTCAGA 489
 1651 GAGTACTCCCTGAAGCTGTGCGGTATACTGAGCCAGGCATCCAAGGCAGG 1700
 490 GAGTACTCCCTGAAGCTGTGCGGTATACTGAGCCAGGCATCCAAGGCAGG 539
 1701 CAAAGTTGTGGACATGCAGGTGAGATCACTGCTCCCTTGCCATTGCCAAC 1750
 540 CAAAGTTGTGGACATG..... 555

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Figure 6B

1751 ATGAGCATTTC AACCTGAGACACGAGAGCTACCTTGCCGATTCAGGAACT 1800
 556CAGGAACT 563
 1801 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCTGGGGTCTG 1850
 564 TTACATGAGGATGACGCTGGACTCCATCTGCAAGGTTGGGTTCTGGGGTCTG 613
 1851 AGATCGGCACGCTGTCTGCCGATCTCCCCGAGAACAGCTTCGCGCAGGCG 1900
 614 AGATCGGCACGCTGTCTGCCAGATCTCCCCGAGAACAGCTTCGCGCAGGCG 663
 1901 TTCGATGCCGCCAACATCATCGTCACGCTGCGGTTTCATCGACCCGCTGTG 1950
 664 TTCGATGCCGCCAACATCATCATCGTCGCGGTTTCATCGACCCGCTGTG 713
 1951 GCGCATCAAGAGGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGA 2000
 714 GCGCATCAAGAGGTTCTTCCACGTCGGGTCAGAGGCCCTCCTAGCGCAGA 763
 2001 GCATCAAGCTCGTGGACGAGTTCACCTACAGCGTGATCCGCCGAGGAAG 2050
 764 GCATCAAGCTCGTGGACGAGTTCACCTACAGCGTGATCCGCCGAGGAAG 813
 2051 GCCGAGATCGTCGAGGCCCGGGCCAGCGGCAAACAGGAGAAGGTACGTGC 2100
 814 GCCGAGATCGTCGAGGTCCGGGCCAGCGGCAAACAGGAGA..... 853
 .
 .
 2201 GCAGATGAAGCACGACATCCTGTACGCTTCATCGAGCTAGGCGAGGCCG 2250
 854 ..AGATGAAGCACGACATCCTGTACGCTTCATCGAGCTGGGCGAGGCCG 901
 2251 GCGACGACGGCGGGCTTCGGGGACGACAAGAGCCTCCGGGACGTGGTG 2300
 902 GCGACGACGGCGGGCTTCGGGGACGATAAGAGCCTCCGGGACGTGGTG 951
 2301 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCTGTG 2350
 952 CTCAACTTCGTGATCGCCGGGCGGGACACGACGGCGACGACGCTGTCTGTG 1001
 2351 GTTCACGCACATGGCCATGTCCCACCCGGACGTGGCCGAGAAGCTGCGCC 2400
 1002 GTTCACGCACATGGCCATGTCCCACCCGGACGTGGCCGAGAAGCTGCGCC 1051
 2401 GCGAGCTGTGCGGTTTCGAGGCGGAGCGCGCGCGAGGAGGGCGTCGCG 2450
 1052 GCGAGCTGTGCGGTTTCGAGGCGGAGCGCGCGCGAGGAGGGCGTCACG 1101
 2451 CTCGTGCCCTGCGGCGGCGCTGACGCCGACGACAAGGCGTTCGCCGCCCG 2500
 1102 CTCGTGCTCTGCGGCGGCGCTGACGCCGACGACAAGGCGTTCGCCGCCCG 1151

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Figure 6C

2501 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 2550
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1152 CGTGGCGCAGTTCGCGGGCCTCCTCACCTACGACAGCCTCGGCAAGCTGG 1201
 2551 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 2600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1202 TCTACCTCCACGCCTGCGTCACCGAGACGCTCCGCCTGTACCCCGCCGTC 1251
 2601 CCTCAGGTGAGCGCGCCCGACACGCGACCTCCGGTCCAGAGCACAGCATG 2650
 ||||
 1252 CCT..... 1254
 2651 CAGTGAGTGACCTGAATGCAATGCACATGCACTTGCGCGCGCGCAGGAC 2700
 |||||
 1255CAGGAC 1260
 2701 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 2750
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1261 CCCAAGGGGATCCTGGAGGACGACGTGCTGCCGGACGGGACGAAGGTGAG 1310
 2751 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 2800
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1311 GGCCGGCGGGATGGTGACGTACGTGCCCTACTCGATGGGGCGGATGGAGT 1360
 2801 ACAACTGGGGCCCCGACGCGGCGAGCTTCCGGCCGGAGCGGTGGATCAAC 2850
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1361 ACAACTGGGGCCCCGACGCGGCGAGCTTCCGGCCGGAGCGGTGGATCAAC 1410
 2851 GAGGATGGCGCGTTCCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 2900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1411 GAGGATGGCGCGTTCCGCAACGCGTCGCCGTTCAAGTTCACGGCGTTCCA 1460
 2901 GGCGGGGCGGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 2950
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1461 GGCGGGGCGGAGGATCTGCCTGGGCAAGGACTCGGCGTACCTGCAGATGA 1510
 2951 AGATGGCGCTGGCCATCCTCTTGCCTTCTACAGCTTCCGGCTGCTGGAG 3000
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1511 AGATGGCGCTGGCCATCCTCTTGCCTTCTACAGCTTCCGGCTGCTGGAG 1560
 3001 GGGCACC CGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 3050
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1561 GGGCACC CGGTGCAGTACCGCATGATGACCATCCTCTCCATGGCGCACGG 1610
 3051 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTG.... 3096
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1611 CCTCAAGGTCCGCGTCTCTAGGGCCGTCTGATGTCATGGCGATTTGGATA 1660
 3097 .GGATATCATCCCGCTTAATCC.....TTAAAAATT 3126
 ||||||| ||||||||| |||||
 1661 TGGATATCGTCCCGCTTAATCCACGACAAATAACGCTCGTGTTACAAATT 1710
 3127 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 3176
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1711 TGCATGCATGCATGTAAGGGAAAGCGATGGGTTTCATTGGTGGCTTGGCT 1760

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Figure 6D

3177 TAAGCCTTAAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 3226
|||||
1761 TAAGCCTTAAAAACTCCGTCGGGTCTTGCGAACCACCACATCACTAGTGT 1810
3227 TTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC 3276
|||||
1811 TTTGTACTCTACTCCTCAGTGGAAGTGTAGTGACAGCATACAAGTTCATC 1860
3277 ATATATATTATCCTCTTTCTTCGCCGGATGCTTCCCGGGACCTTTTGGAG 3326
|||||
1861 ATATATATTATCCTCTTTCTTAAAAAAAAAAAAAAAAAACTCGAG.... 1906

...

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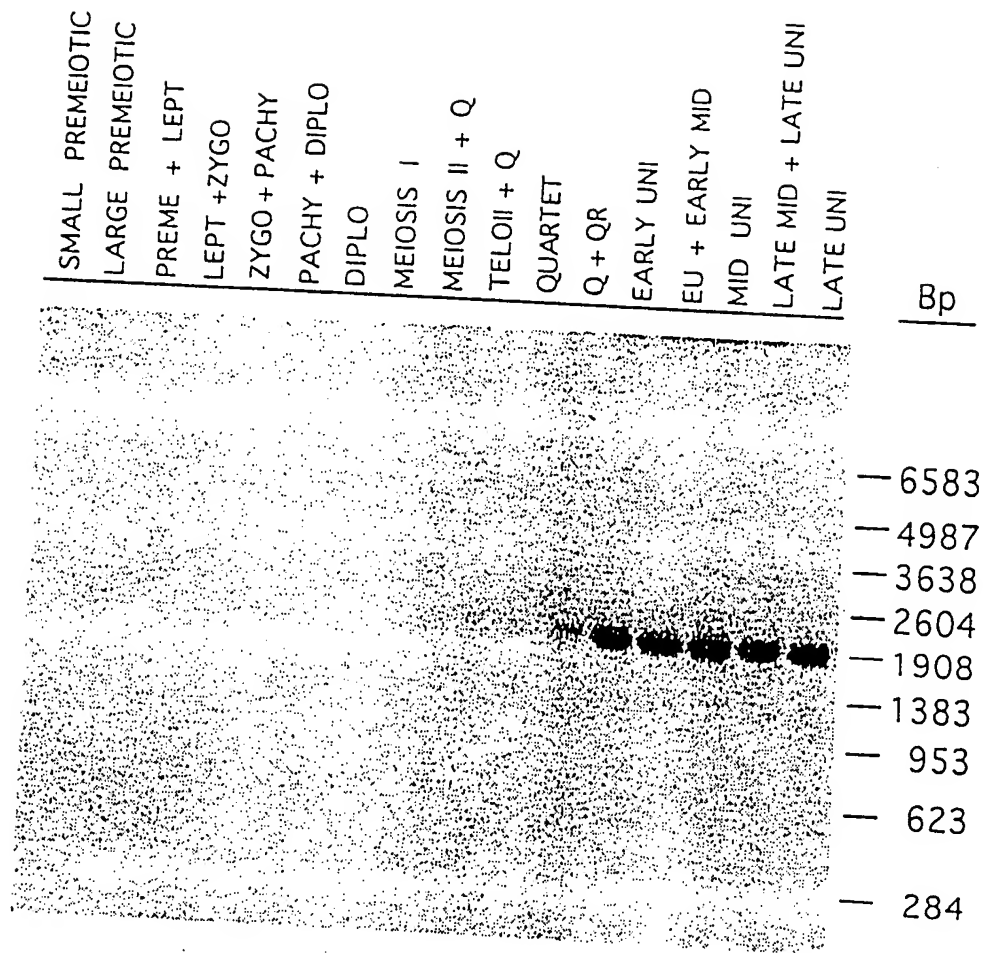


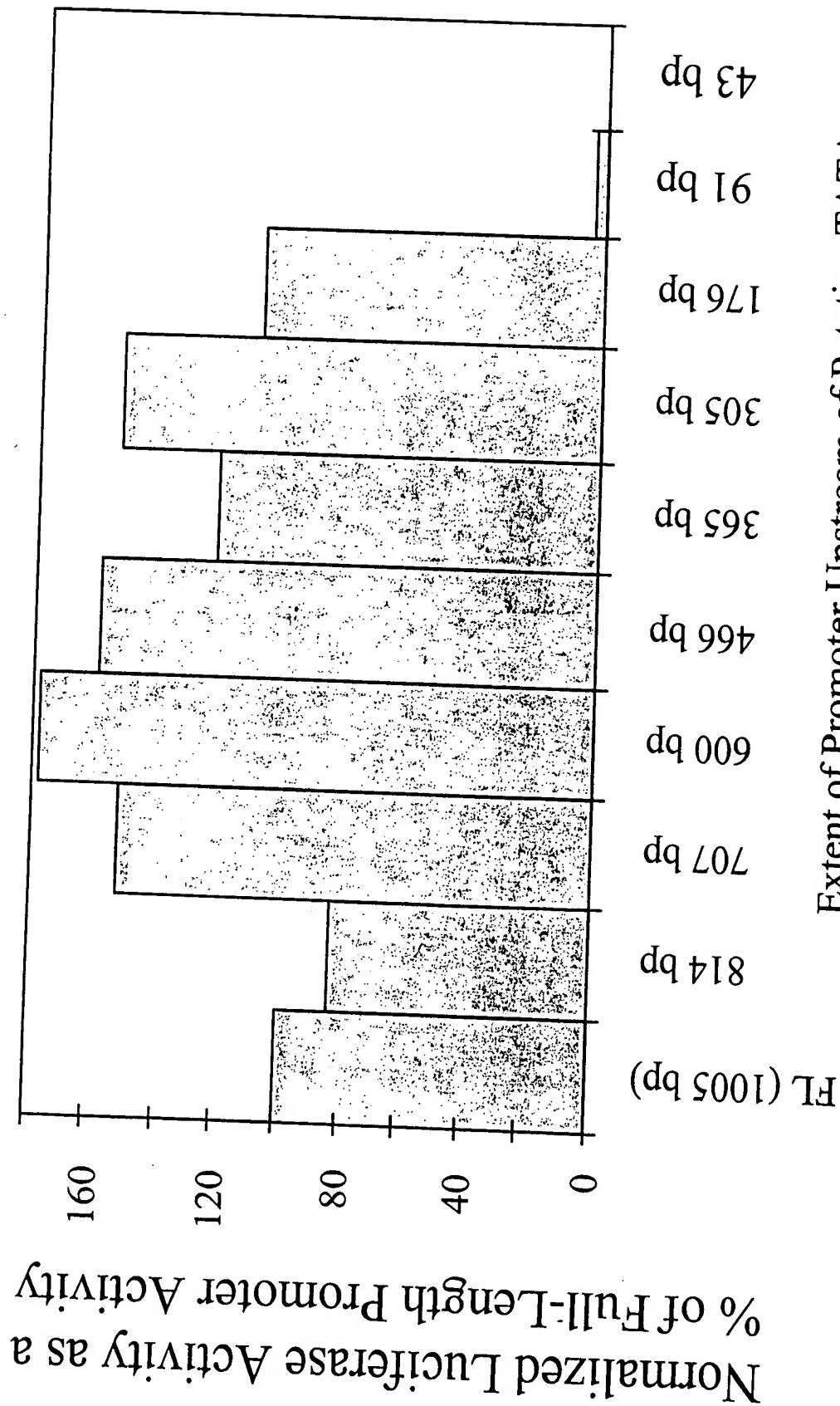
Figure 7

Figure 8

1 GAATTCCAAG CGAGGCCCTT GTAGCAGAGA GTGTTGCTGA TGCAGTCGGC
51 GGAAATGAGT GCGTGCTGAG AGCAACGCTG AGGGGTTCCA GGGATGGCAA
101 TGGCTATGGC AATCGGCTAG AGGTGGAGGA CAAGGTGGTG AGGATTGGGA
151 GGGCAACCTA TGGCAAGTTG GTGAAGAGGC ACGCAATGAG AGATCTATTC
201 AGACTTACAC TGGATGCCGC CAACAAATTC AACCTTTAGA TTTTGATACT
251 GTCACTCCTA CTTTATTCCT TGGTTGGGCA ACTTCCAATA GGCTCATGTT
301 AATCAATGAT TAGTGATTAT TCAGCAAATA TTCTTGTTTG TTTGACATTT
351 ATAATATGTG GGGTGAGACG GATTAAATAT CATCCATGAG AGCTTTATCT
401 TCATGCTCTC TTGATTTTGG TTTCAGATCA TTCTTTCAGT GTTCACAAGA
451 ATTTTCTCAG TTTGGTCCAT GTAATTTTGG AAGTGAGGTT CCTTAAATTT
501 CATTATGCTT CCTTTCTTTT CTAGACTAGC AACTGCATGA CTTTTCACCT
551 TGGGTTTACA AATTGACTCA CAAGAAAACA AATTCACCTT TGGGTTTACA
601 AATTCCTCTT CAGGATGTAC TTTTCACTTG AACTGTCATG TATAGGAACA
651 AGGAATGGCT CAGTTTTTAA GGAACAATGT ACAGATTTCA TTTCAGAACT
701 CTTTCTGGTT GGTGAGTTT CAGACTTTTT GTACCAAGCT GATGGATCAC
751 AATACTTGTT TCCAAAGTCT GATAACAGAA ACTGGCAACT CCTAATTGAT
801 AATAAAAAGA ATAAAATACA GTATCAGATA TCTCATTTTC TTGGTTGGCA
851 GATCACAAAA AGGAACACAA AGGCTAAGCC TCCTACTTGT TCGGGAGTTA
901 GGTCAGGGAC ACCATATGAA TGAAAGAAAT CTTAATTGG GGTACACCA
951 AGATTGTCTC TCTCGAGGTT GGGGGTCCC TAAGGTTGGT AGTAGCAATA
1001 CCCAATATAT CACCTAACAA ACCCAATCCA TGCTACATAC ATACATAGCA
1051 TCCATCACTT GTAGACTGGA CCCTTCATCA AGAGCACCAT GG

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SBMu200 Promoter Analysis: 5' Deletions



Extent of Promoter Upstream of Putative TATA
Figure 9

SBMu200 "Minimal" Promoter

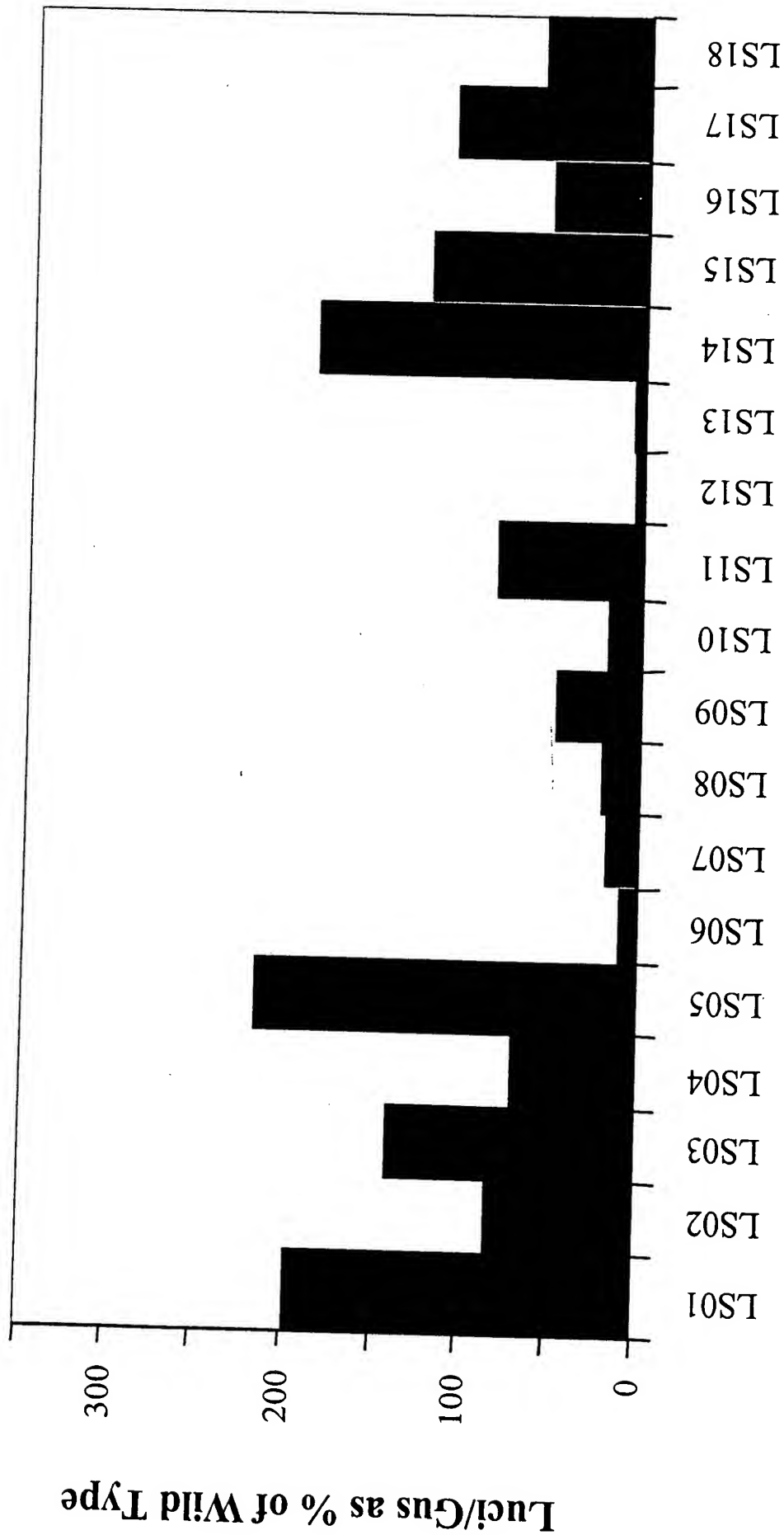
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-180 CCCATCTCA TTTTCTTGGT TGGCAGATCA CAAAAGGAA CACAAAGGCT
      LS01 | LS02 | LS03 | LS04 | LS05 |
-130 AAGCCTCCTA CTTGTTTCGG AGTTAGGTCA GGGACACCAT ATGAATGAAA
      LS06 | LS07 | LS08 | LS09 | LS10 |
-80  GAAATCTTAA TTGGGGGTCA CACCAAGATT GTCTCTCTCG AGGTGCGGG
      LS11 | LS12 | LS13 | LS14 | LS15 |
-30  GTCCCTAAGG TTGGTAGTAG CATTACCCTA TATATCACCT AACAAACCCA
      LS16 | LS17 | LS18 |
20  ATCCATGCTA CATACATACA TAGCATCCAT CACTGTAGA CTGGACCCTT
70  CATCAAGAGC ACCATGG
  
```

Coordinates are relative to the putative TATA box (underlined). P motifs are in *italic*.
 [] = Del -176/-92 [] = Del -89/-44 [] = Del -39/-8
 Linker scanning mutations that reduce activity to ~5% or less are in **bold**. Mutations
 with a significant but less pronounced effect are in *bold italic*.

Figure 10

Linker Scanning Analysis of SBMu200 Promoter



Mutant

Figure 11

Figure 12

1GGAA 4
 201 CCGGATGCACGACTGGCTTGTCTGGGTACCTGTACGGCACAGGACAGTGA 250
 5 TTCGGCTTATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT 54
 251 CCGTCGACATGCCGTTCACTTCCTACACCTACATCGCTGACCCGGTGAAT 300
 55 GTCGAGCATGTCTCAAGACTAAGTTCACCAATTACCCAAGGGGGACGT 104
 301 GTCGAGCATGTCTCAAGACTAAGTTCACCAATTACCCAAGGGAATCGT 350
 105 GTACAGATCCTACATGGATGTGCTCCTCGGTGACGGCATATTCAACGCTG 154
 351 GTACAGATCCTACATGGACGTGCTCCTCGGTGACGGCATCTTCAACGCCG 400
 155 ACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTTTCGAGTTCGCC 204
 401 ACGGCGAGCTGTGGAGGAAGCAGAGGAAGACGGCGAGTTTCGAGTTCGCC 450
 205 TCCAAGAACCTGAGGGATTTCACTGCCAATGTTTTTCAGAGAGTACTCCCT 254
 451 TCCAAGAACCTGAGGGATTTCACTGCCAATGTTTTTCAGAGAGTACTCCCT 500
 255 GAAGCTGTCTGGGCATACTGAGTCAGGCATCCAAGGCAGGCAAAGTTGTTG 304
 501 GAAGCTGTCTGGGTATACTGAGCCAGGCATCCAAGGCAGGCAAAGTTGTTG 550
 305 ACATGCAGGAACCTTTACATGAGGATGACACTGGACTCGATCTGCAANGTT 354
 551 ACATGCAGGAACCTTTACATGAGGATGACGCTGGACTCCATCTGCAAGGTT 600
 355 GGGTTCGGGGTCNANATCGGCACGCTGTCTCCGGATCTCCCGAGAACAG 404
 601 GGGTTCGGGGTCGAGATCGGCACGCTGTCTCCAGATCTCCCGAGAACAG 650
 405 CTTNCCCCAAGCGTTTCGATGCCGCTAACATCATCGTCACNCTGCGGTTCA 454
 651 CTTGCGCAGGCGTTTCGATGCCGCTAACATCATCATCAGCTGCGGTTCA 700
 455 TCCACCCNCTGTGGCGCATCCAGAAGTTCTTCCCNGTCA..... 494
 701 TCGACCCGCTGTGGCGCATCAAGAGGTTCTTCCACGTCTGGGTGAGAGGCC 750

Percent Similarity: 92.510 Percent Identity: 90.891
 Sb200-Sorghr.Pep x Sb20081.Pep February 13, 1997 11:29 ..

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 87 MPFTSYTYIADPVNVEHVLKTNFTNYPKGIYRSYMDVLLGDGIFNADGE 136
 55 LWRKQRKTASFEFASKNLRDFSANVFREYSLKLSGILSQASKAGKVVDQM 104
 137 LWRKQRKTASFEFASKNLRDFSIVFREYSLKLSGILSQASKAGKVVDQM 186

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